

SUPPLEMENTARY MATERIAL:

Simulation of multiple ion channel block provides improved prediction of compounds' clinical torsadogenic risk

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1 Experimental Protocols

For the I_{Na} experiments HEK-293 cells stably transfected with hNav1.5 cDNA were continuously maintained in a humidified, gassed ($\sim 5\%$ CO_2) incubator at approximately $37^\circ C$, and passaged using Dulbecco's Modified Eagle Medium (DMEM) supplemented with 10% foetal bovine serum, 1% non-essential amino acids, 1% penicillin/streptomycin and 0.4 mg/mL geneticin. For the I_{CaL} experiments myocytes were isolated enzymatically from guinea-pig ventricle as previously described²¹. Briefly, male guinea-pigs were killed by cervical dislocation following stunning. Myocytes were isolated after perfusion of the heart with a physiological salt solution containing reduced calcium and 0.8 mg/mL of collagenase Type 1 (Worthington Biochemicals). Cells were stored at room temperature in Dulbecco's MEM (Life Technologies, Scotland) and used for electrophysiological investigation on the day of preparation. For the I_{Kr} experiments HEK-293 cells stably transfected with hERG cDNA were obtained from the University of Wisconsin. The cells were continuously maintained in, and passaged, using minimum essential medium supplemented with 10% foetal bovine serum, 1% non-essential amino acids, 1% sodium pyruvate, 1% penicillin/Streptomycin and 0.4 mg/ml geneticin. The cells were seeded onto glass coverslips in 35 mm² dishes (containing 3 ml medium without geneticin) at a density that enabled isolated cells to be selected for patch-clamping.

The conventional whole-cell patch-clamp configuration was used to record membrane currents at room temperature via AxoPatch 200B preamplifiers, and data acquisition and analysis were controlled by Axon pClamp software.

For the I_{CaL} experiments, the composition of the bath solution was (in mM): NaCl 125; $NaHCO_3$ 25; KCl 5.4; $CaCl_2$ 1.8; $MgCl_2$ 1.0; NaH_2PO_4 1.2; D-glucose 5.5; CsCl 5.0; pH 7.4 when bubbled with 95% O_2 and 5% CO_2 ; the composition of the pipette solution was (mM): CsCl 120; TEACl 20; $MgCl_2$ 5.5; EGTA 5.0; ATP-Na2 5.0, HEPES 20; phosphocreatine 5.0; pH 7.2 with 1M CsOH.

For the I_{Na} experiments, the composition of the bath solution was (mM): NaCl 40; CsCl 97; KCl 4.0, $CaCl_2$ 1.8; $MgCl_2$ 1.0; D-glucose 10; HEPES 10; pH 7.4 with 1M CsOH; the composition of the pipette solution was (mM): CsCl 130; $MgCl_2$ 5.0; EGTA 5.0; MgATP 4.0; GTP 0.1, HEPES 10; pH 7.2 with 1M CsOH.

The voltage protocols for studying the concentration-dependent effect of the compounds on peak current were as follows. For I_{Na} , a step from -100 mV (holding potential) to -30 mV for 20 ms, then step back to a holding potential of -100 mV. For I_{CaL} , a step from -40 mV (holding potential) to 0 mV for 400 ms, and then stepped back to the holding potential of -40 mV. The pulses were applied at frequencies of 0.1 and 0.2 Hz for I_{Na} and I_{CaL} respectively. Peak I_{Na} was measured with respect to the holding current measured at -100 mV just before the step depolarisation and peak I_{CaL} amplitude was measured relative to the holding current at -40 mV. For I_{Kr} , the holding potential was -80 mV. The step from -80 mV to the test command ($+20$ mV, 5 s) activated hERG channels and the step from the test command ($+20$ mV) to -50 mV (5 s) resulted in the tail current, whose amplitude was measured. The testing pulses were applied at 15 s intervals. These protocols were used to construct concentration-response curves.

Experiments were performed at Safety Pharmacology, GlaxoSmithKline. The investigation conforms with the Guide for the Care and Use of Laboratory Animals published by the US National Institutes of Health (NIH Publication No. 85-23, revised 1996). All animals were treated in accordance with UK Home Office regulations (Animals (Scientific Procedures) Act 1986: London: Her Majesty's Stationery Office 1986) and the work was approved by internal ethical review.

2 Simulation Protocols

In this section we describe the three protocols under which the models were used to simulate cellular responses, and state the model outputs that we have taken as potential *in-silico* risk indicators. We correlated these markers against the TdP risk categories as described in section 2.4 of the main text and section 3.1 of this document, in order to establish those markers that provided an indication of risk.

Firstly, we considered the membrane voltage under regular pacing. Models were paced at 1Hz for 1000 seconds in order to obtain an approximately steady behaviour. The final AP was analysed and the maximum upstroke velocity (proportional to peak current), peak membrane voltage, and APD at 50% and 90% repolarisation were recorded, along with APD90 minus APD50 as measure of ‘triangulation’. The cytosolic calcium transient corresponding to this AP was also analysed; peak calcium, 50% duration, 90% duration and triangulation of the transient were recorded.

Secondly, the S1-S2 restitution protocol, was performed on the models. 1Hz was chosen as the S1 pacing frequency and the models were again paced for 1000 seconds in order to obtain a steady state before the protocol began. Results were analysed to determine the maximum slope of the restitution curve.

Finally, a dynamic restitution protocol was performed. This consisted of 100 paces at varying frequencies from 1Hz up to 10Hz. The final eight action-potential traces at each frequency were analysed to detect voltage alternans and the frequency at which depolarisation occurred before 90% repolarisation had completed (i.e. the frequency at which non-spontaneous EADs were induced), the highest pacing cycle length at which either occurred was recorded as the ‘instability onset’. The maximum slope of the dynamic restitution curve was recorded. The area between the control and drug-blocked dynamic restitution curves was also recorded; this measure is intended to quantify the change in APD over a range of pacing frequencies.

The full list of the 15 simulated markers is:

1. Steady-State 1Hz pacing
 - APD90
 - APD50
 - APD Triangulation
 - Peak membrane voltage
 - Maximum upstroke velocity
 - Ca duration 90
 - Ca duration 50
 - Ca triangulation
 - Peak Ca

2. S1-S2 Restitution

- Maximum slope

3. Dynamic Restitution

- Maximum slope
- Alternans onset pacing frequency
- (non-spontaneous) EAD onset frequency
- Instability onset frequency
- Area between control and drug curves

The tolerances of CVODE were set as: relative, 10^{-5} ; absolute, 10^{-7} . The simulations involved in determining the 1Hz APD90 for the Grandi *et al.* model for a compound at a particular concentration, and the subsequent classification of the compound into a risk category, can be completed in under one minute on a single core of a desktop PC (an Intel Core2 Duo 3GHz desktop PC was used). We propose that the calculation be performed for a range of concentrations, informing the therapeutic doses at which the compound may be used safely.

3 Details of Statistical Methods

In this section we provide more details on the statistical methods used to evaluate the predictive power of the different markers. Section 3.1 provides details of the implementation of the LDA technique, and section 3.2 provides details of validation techniques used to ensure that the predictive power of our markers was not down to chance.

3.1 Linear Discriminant Analysis Implementation

We assemble a large matrix of training data \mathbf{X} from distinct categories $k = 1 \dots K$ (in our case $K = 4$ — the number of risk categories after combining 1 and 2 due to their equal risk). Each row i of \mathbf{X} represents a drug, and each column j contains a ‘discriminant variable’ — one of our measures (e.g. hERG IC50 or simulated APD90 from a particular model). Here we follow the notation of Hastie *et al.*⁸⁰, to whom we refer the interested reader to their section 4.3 for a full derivation of this technique.

Our prior distributions (the likelihood that a drug belongs to a particular category) are set equal and given as

$$\pi_k = 1/K, \quad (1)$$

If the mean value of our measures for the training points in category k is denoted by the vector μ_k , then the ‘pooled’ or ‘common’ covariance matrix is given by

$$\Sigma = \sum_{k=1}^K \sum_{\forall i \in k} (\mathbf{X}_i - \mu_k) (\mathbf{X}_i - \mu_k)^T / (N - K). \quad (2)$$

where N is the total number of drugs and \mathbf{X}_i is a vector of measures for a particular drug. The linear discriminant functions for each category are then given by

$$\delta_k(y) = y^T \Sigma^{-1} \mu_k - \frac{1}{2} \mu_k^T \Sigma^{-1} \mu_k + \ln \pi_k. \quad (3)$$

A new observation y is then classified to the category k for which the discriminant function $\delta_k(y)$ is largest. Notice that for the 1D markers presented in the main text \mathbf{X}_k is a column vector. We demonstrate briefly how this method works in Figure S1.

In the bottom panel of Figure S1 we see a set of training data from four distinct categories, distributed along a one dimensional variable ‘ y ’. LDA is derived based on the assumption that the training data in each category are normally distributed, with each category having a different mean but a common covariance matrix. Our dataset is not large enough to test whether the points in each category follow a normal distribution, yet in practice LDA has been found to work well for many distributions⁸⁰. LDA then uses maximum likelihood estimates to calculate the probability of each point in y -space being a member of each category. The resulting probability of an unseen observation belonging to each of the categories is shown in the top panel of Figure S1. To classify an unseen observation we simply assign it to the category with the highest probability at that point.

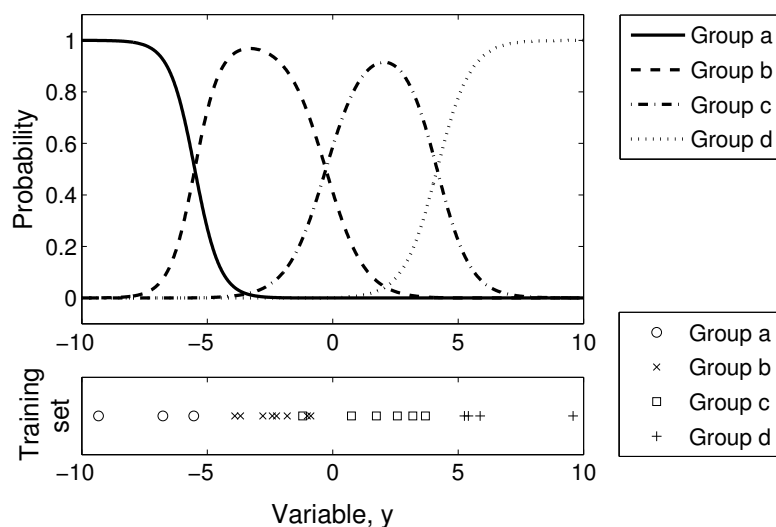


Figure S1: An example of how linear discriminant analysis classifies points in variable space into distinct categories. Bottom: a set of 1D training variables taken from four distinct categories. Top: the probability of being classified into each category at each point in (1D) variable space, each point in variable space would be classified into the category k with the largest discriminant function $\delta_k(y)$ (or equivalently probability) at that point.

3.2 Cross-validation

Despite the fact that the errors in classification as shown in Figure 4 of the main text are entirely independent of the training data (because of the N-fold cross validation/‘leave-one-out validation’), a possible criticism of our approach would be that we tried many different markers, and the success of the best-performing one was purely by chance. We have evaluated the predictive power that such ‘random guesses’ for the categories would provide. In Figure S2 we plot the resulting error for 1,000; 10,000; 100,000 and 1,000,000 random guesses: none of the resulting errors are as small as those of the simulated marker suggested in the main text. This finding suggests that the measure has strong predictive power and has not been successful ‘by chance’.

The fact that the distribution shown in Figure 5 in the main text shows a clear bias towards “being predictive”, rather than “being random” (as plotted in Figure S2) provides further evidence that our approach is indeed producing predictive power and our findings are not a chance result. Indeed the 30 “most predictive” markers listed in Supplementary Material 4, and shown in bold on Figure 5 of the main text, are all multi-channel markers. None of the hERG-only markers were as accurate, providing further evidence that the multichannel simulations are not outperforming the existing measures by chance.

Yet, we acknowledge that the choice of best marker was strongly dependent on the dataset. In order to ascertain whether our measure of Grandi *et al.*²⁶ APD90 was robust to the different datasets of drugs we split them into separate groups for K-fold cross validation of the marker choice. Although Hastie *et al.*⁸⁰ suggest that K is

generally taken to be between 5 and 10 we use $K = 4$ because we only have four drugs in category 2.

1. Quinidine (1), Ajmaline (1), Cisapride (2), Pimozide (3), Fluvoxamine (4), Mibefradil (4), Risperidone (5), Nitrendipine (5).
2. Amiodarone (1), Terfenadine (2), Sertindole (3), Bepridil (3), Desipramine (4), Amitriptyline (4), Nifedipine (4), Cibenzoline (5), Verapamil (5).
3. Dofetilide (1), Prenylamine (2), Chlorpromazine (3), Diphenhydramine (4), Imipramine (4), Phenytoin (5), Propranolol (5).
4. Tedisamil (1), Thioridazine (2), Haloperidol (3), Propafenone (4), Mexiletine (4), Quetiapine (4), Diltiazem (5).

These groups were chosen so that each contained roughly equal numbers of drugs from each of the risk categories (as shown in brackets after the drug name). The stratified training datasets were then formed by ‘leave-one-group-out’: so stratification set 1 was formed from groups 2, 3, 4, stratification set 2 from groups 1, 3, 4 etc. This was necessary to ensure that each risk category contained a number of points with which to ‘train’ the LDA method.

The method referred to in the main text (individual ‘leave-one-out’ for each compound, LDA, and finally classification) was then performed for each of these stratified training datasets. We subsequently ranked the predictive power of each marker in each of the training datasets.

In Figure S3 we present the same data as in the main text’s Figure 5 for each of the stratified datasets. The top 30 markers for the full dataset are again shown in bold. We see that the most predictive measures are relatively robust across the different stratifications, and in particular our best measure Grandi *et al.*²⁶ APD90 (as designated by the dotted lines) consistently outperforms both the existing measure (dashed lines) and random guesses (solid lines).

In addition to the experiment displayed in the main text we also performed a 2D LDA analysis for every combination of the 761 1D markers (289180 in total). The result of this was a slight improvement over the 1D markers (as shown in Figure S4), but a possible loss of consistency between stratified groups as shown in Figure S5 (it is possible that out of so many markers “predictive” ones appear by chance, as shown in Figure 2(c) for 100,000 random category guesses). For this reason the main text refers only to the more robust 1D markers.

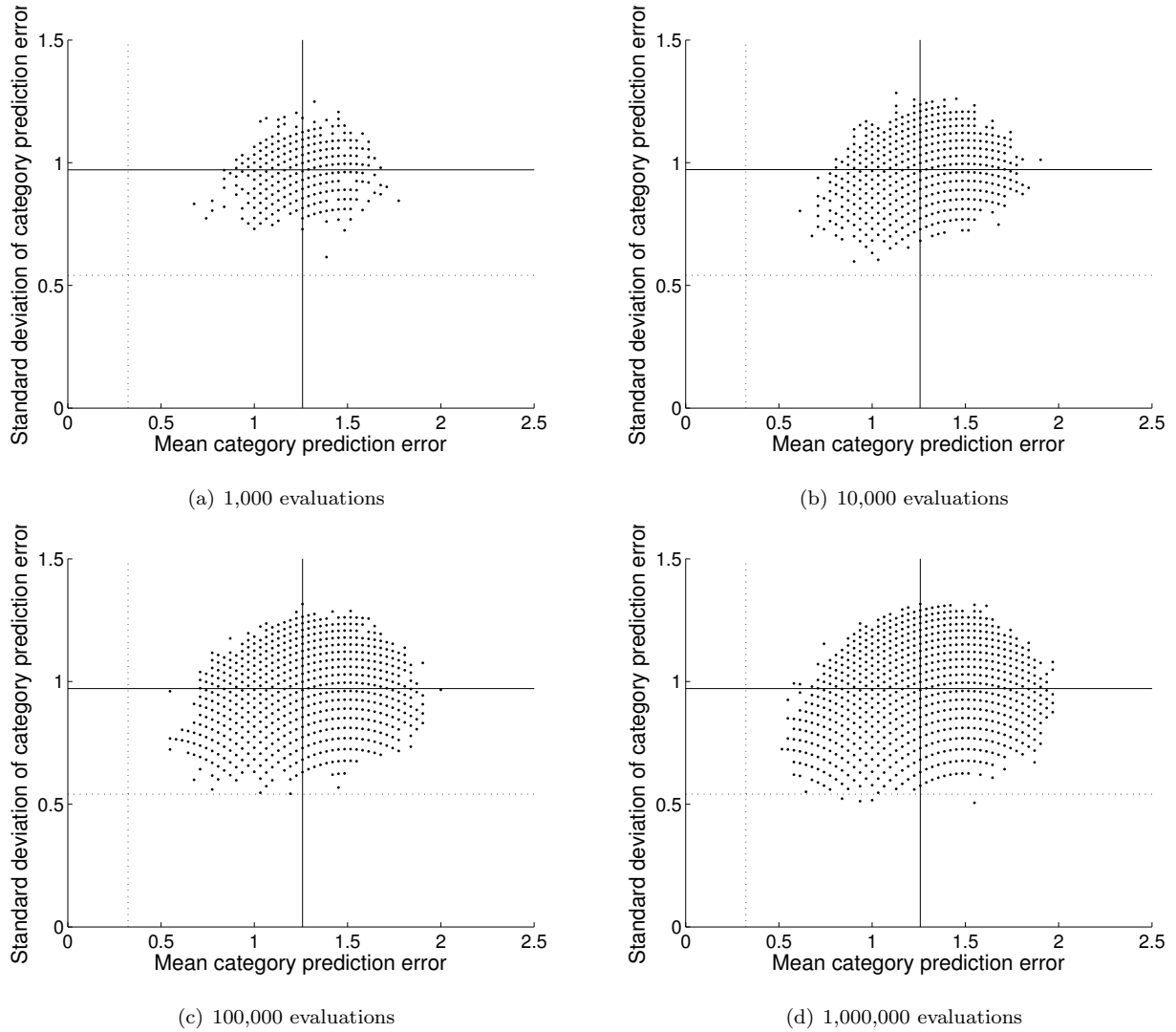


Figure S2: Classification errors resulting from (a) 1,000; (b) 10,000; (c) 100,000; and (d) 1,000,000 sets of random guesses for the drug risk categories. The mean values on each plot are given by solid lines, and the errors given by the 1D simulated marker (Figure 5 in the main text) are shown by dashed lines. It appears that categorisation at random has far less than 1 in a million chance of performing as well as the simulated marker. The ‘patterns’ arise because there are a limited number of possible mean and standard deviations in errors with a fixed number of drugs.

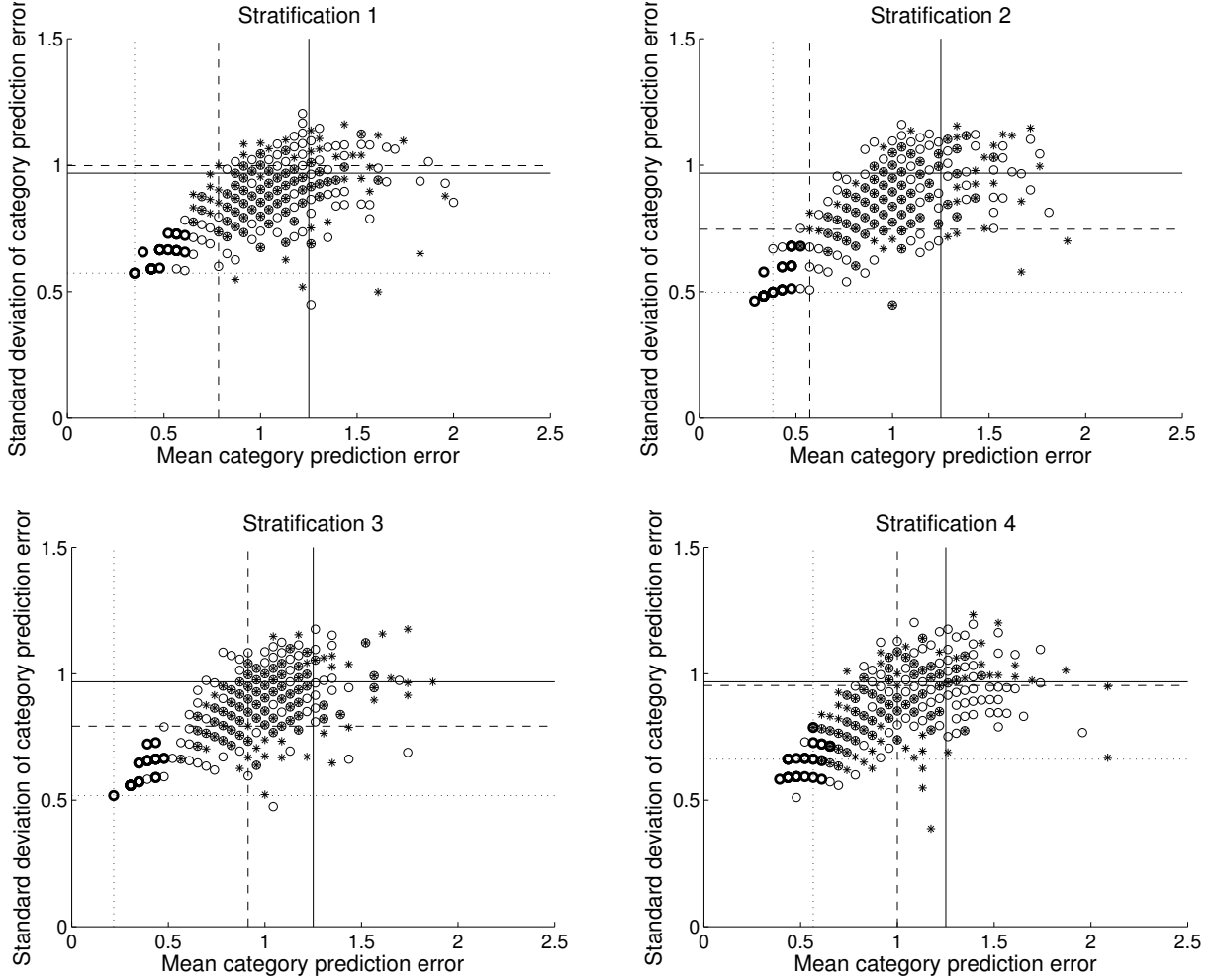


Figure S3: Scatter plot of classification error for all of the different markers for stratified datasets. The most predictive markers for the full dataset, as shown in bold in Figure 5 of the main text, are again shown here in bold for the four stratified datasets. Simulated markers from hERG-only block are denoted with ‘*’ whilst multichannel block markers are denoted by ‘o’. Solid lines indicate the expected values if classification was performed at random, dashed lines are the values given by $\log_{10}([\text{hERG IC}_{50}]/[\text{EFTPC High}])$, dotted lines are the values for the longest APD90 from simulations of Grandi *et al.*²⁶ at low/med/high EFTPC, it provides a consistent improvement over the existing safety factor.

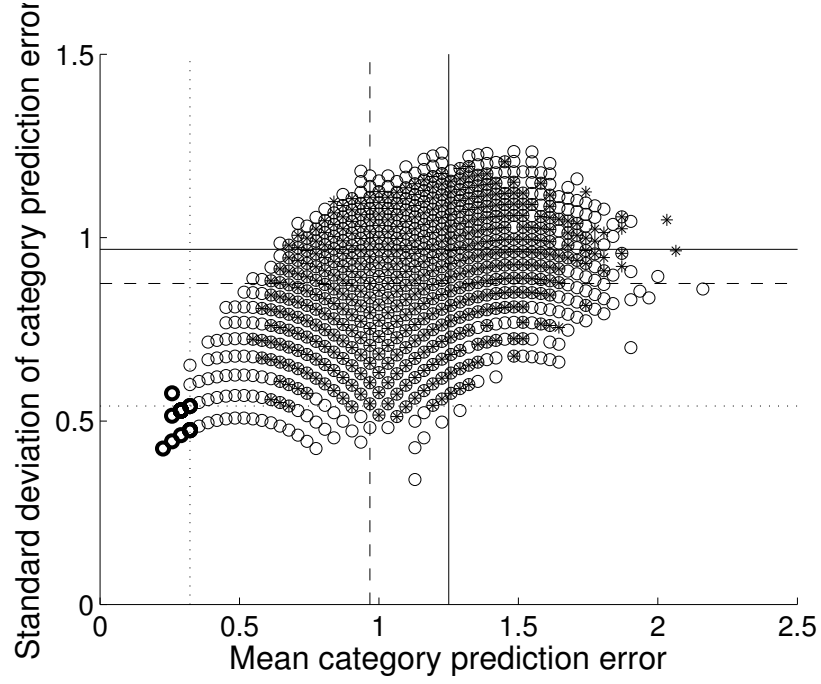


Figure S4: Scatter plot of classification error for all of the different 2D markers. Simulated markers where both are from hERG-only block are denoted with ‘*’ whilst multichannel block or mixed markers are denoted by ‘o’. Solid lines indicate the expected values if classification was performed at random, dashed lines are the values given by $\log_{10}([\text{hERG IC}_{50}]/[\text{high EFTPC}])$, dotted lines are the values given by the best 1D marker as shown in Figure 3(b) of the main text . Again, all of the 30 most predictive 2D markers result from multichannel simulations and these are denoted with bold markers.

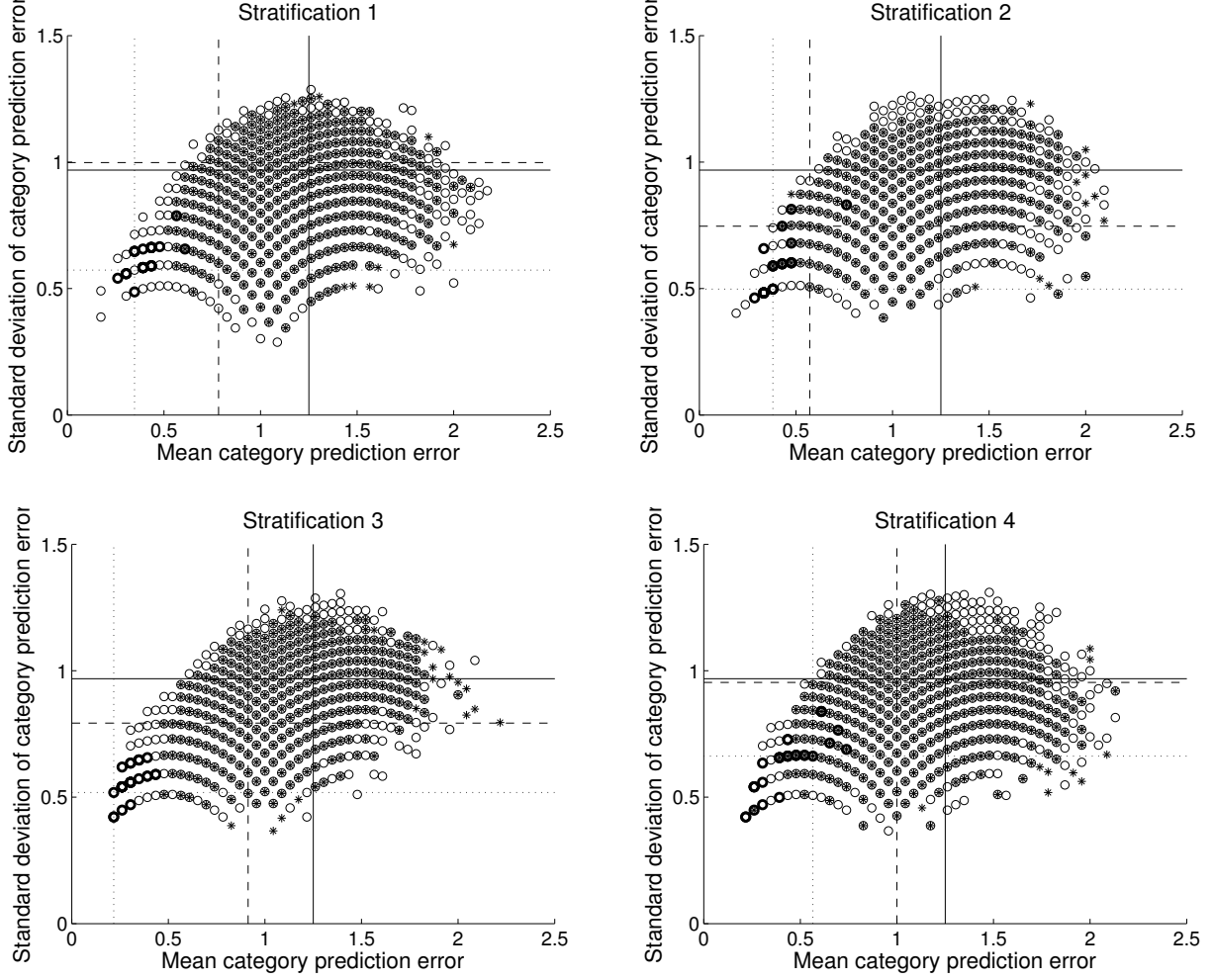


Figure S5: Scatter plot of classification error for all of the different 2D markers for stratified datasets. The most predictive markers for the full dataset, as shown in bold in Figure S4 of the main text, are again shown here in bold for the four stratified datasets. Where both simulated markers are from hERG-only block they are denoted with ‘*’ whilst multichannel block or mixed markers are denoted by ‘o’. Solid lines indicate the expected values if classification was performed at random, dashed lines are the values given by $\log_{10}([\text{hERG IC}_{50}]/[\text{EFTPC High}])$, dotted lines are the values from the 1D measure (the longest APD90 from simulations of Grandi *et al.*²⁶ at low/med/high EFTPC).

4 Most predictive markers

The 30 most predictive markers resulting from the LDA leave-one-out trial are shown in Table S1. Notice that all are from multi-channel block simulations, and the majority are measures associated with AP prolongation. All of these markers provide risk predictions which have less than half of the error in classification that the current best-practise marker exhibits, as shown in Figure 5 of the main text.

Error in category		Discriminant Measure
Mean	Std. Dev.	
0.323	0.541	Grandi <i>et al.</i> APD90 EFTPC with largest effect
0.355	0.551	Shannon <i>et al.</i> (2004) Peak Ca EFTPC with largest effect
0.387	0.558	Shannon <i>et al.</i> (2004) APD50 Medium EFTPC
0.387	0.615	Shannon <i>et al.</i> (2004) Dynamic EAD Start Freq EFTPC with largest effect
0.419	0.564	ten Tusscher & Panfilov (2006) APD50 Medium EFTPC
0.419	0.620	Shannon <i>et al.</i> (2004) Peak Ca High EFTPC
0.419	0.620	Shannon <i>et al.</i> (2004) Dynamic Max Slope EFTPC with largest effect
0.419	0.620	Shannon <i>et al.</i> (2004) Dynamic Area Between Curves High EFTPC
0.419	0.620	Hund & Rudy (2004) Dynamic Alternans Start Freq EFTPC with largest effect
0.419	0.620	Hund & Rudy (2004) Dynamic Instability Onset Freq EFTPC with largest effect
0.419	0.620	Grandi <i>et al.</i> (2010) Dynamic Area Between Curves Medium EFTPC
0.419	0.672	Shannon <i>et al.</i> (2004) APD50 High EFTPC
0.419	0.672	Shannon <i>et al.</i> (2004) Dynamic EAD Start Freq Medium EFTPC
0.419	0.672	Grandi <i>et al.</i> (2010) Dynamic Area Between Curves High EFTPC
0.452	0.568	Shannon <i>et al.</i> (2004) APD90 Medium EFTPC
0.452	0.568	Shannon <i>et al.</i> (2004) Peak Ca Medium EFTPC
0.452	0.568	Shannon <i>et al.</i> (2004) Dynamic Area Between Curves Medium EFTPC
0.452	0.568	Grandi <i>et al.</i> (2010) Dynamic Area Between Curves EFTPC with largest effect
0.452	0.624	Shannon <i>et al.</i> (2004) APD90 High EFTPC
0.452	0.624	Shannon <i>et al.</i> (2004) Dynamic Area Between Curves EFTPC with largest effect
0.452	0.624	ten Tusscher & Panfilov (2006) APD90 High EFTPC
0.452	0.624	ten Tusscher & Panfilov (2006) APD50 High EFTPC
0.452	0.624	ten Tusscher & Panfilov (2006) Dynamic Area Between Curves Medium EFTPC
0.452	0.624	Hund & Rudy (2004) Dynamic Instability Onset Freq Low EFTPC
0.452	0.624	Grandi <i>et al.</i> (2010) APD50 EFTPC with largest effect
0.484	0.570	Shannon <i>et al.</i> (2004) CaD90 Medium EFTPC
0.484	0.626	Shannon <i>et al.</i> (2004) APD90 EFTPC with largest effect
0.484	0.626	Shannon <i>et al.</i> (2004) APD50 EFTPC with largest effect
0.484	0.626	ten Tusscher & Panfilov (2006) APD90 Medium EFTPC
0.484	0.626	Hund & Rudy (2004) Dynamic Instability Onset Freq Medium EFTPC

Table S1: The 30 most predictive 1D measures, as highlighted in bold in Figure 5 of the main text. All are multi-channel simulated markers.

5 Classification Errors

The errors in Table S2 resulted from leave-one-out, linear discriminant analysis, when classifying according to Grandi *et al.* largest APD90 at any EFTPC.

Generic Drug Name	APD90 Change (ms)	Risk Category		Error (categories)
		Actual	Predicted	
Ajmaline	2.37	2	3	1
Amiodarone	0.37	2	4	2
Dofetilide	12.51	2	2	0
Quinidine	26.68	2	2	0
Tedisamil	1.40	2	3	1
Cisapride	19.71	2	2	0
Prenylamine	6.75	2	3	1
Terfenadine	18.01	2	2	0
Thioridazine	18.31	2	2	0
Bepidil	2.82	3	3	0
Chlorpromazine	1.14	3	3	0
Haloperidol	4.62	3	3	0
Pimozide	1.26	3	3	0
Sertindole	4.24	3	3	0
Amitriptyline	-0.01	4	4	0
Desipramine	-1.27	4	4	0
Diphenhydramine	0.22	4	4	0
Fluvoxamine	-0.28	4	4	0
Imipramine	-0.12	4	4	0
Mexiletine	-0.60	4	4	0
Mibefradil	-5.21	4	4	0
Nifedipine	-6.91	4	5	1
Propafenone	0.38	4	4	0
Quetiapine	-0.09	4	4	0
Cibenzoline	-0.85	5	4	1
Diltiazem	-14.36	5	5	0
Nitrendipine	-29.51	5	5	0
Phenytoin	-3.35	5	4	1
Propranolol	0.31	5	4	1
Risperidone	0.51	5	4	1
Verapamil	-20.75	5	5	0

Table S2: Classification errors resulting from use of the most predictive measure, there are compiled into a histogram to make Figure 4(d) in the main text.

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